

(i) APPLICANT: Mathews, Lawrence S.
Vale, Wylie W.
Tsuchida, Kunihiro

(ii) TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Los Angeles

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/300,584

(B) FILING DATE: 02-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/880,220

(B) FILING DATE: 08-MAY-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/773,229

(B) FILING DATE: 09-OCT-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/698,709

(B) FILING DATE: 10-MAY-1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.

(B) REGISTRATION NUMBER: 31,192

(C) REFERENCE/DOCKET NUMBER: P41 9927

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2563 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

CTCCGAGGAA	GACCCAGGGA	ACTGGATATC	TAGCGAGAAC	TTCCTACGGC	TTCTCCGGCG	60
CCTCGGGAAA	ATG GGA GCT GCT GCA AAG TTG GCG TTC GCC GTC TTT CTT	109				
Met	Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu					
1	5	10				
ATC TCT TGC TCT TCA GGT GCT ATA CTT GGC AGA TCA GAA ACT CAG GAG	157					
Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu						
15	20	25				
TGT CTT TTC TTT AAT GCT AAT TGG GAA AGA GAC AGA ACC AAC CAG ACT	205					
Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr						
30	35	40	45			
GGT GTT GAA CCT TGC TAT GGT GAT AAA GAT AAA CGG CGA CAT TGT TTT	253					
Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe						
	50	55	60			
GCT ACC TGG AAG AAT ATT TCT GGT TCC ATT GAA ATA GTG AAG CAA GGT	301					
Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly						
	65	70	75			
TGT TGG CTG GAT GAT ATC AAC TGC TAT GAC AGG ACT GAT TGT ATA GAA	349					
Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu						
	80	85	90			
AAA AAA GAC AGC CCT GAA GTG TAC TTT TGT TGC TGT GAG GGC AAT ATG	397					
Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met						
95	100	105				
TGT AAT GAA AAG TTC TCT TAT TTT CCG GAG ATG GAA GTC ACA CAG CCC	445					
Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro						
110	115	120	125			
ACT TCA AAT CCT GTT ACA CCG AAG CCA CCC TAT TAC AAC ATT CTG CTG	493					
Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu						
	130	135	140			
TAT TCC TTG GTA CCA CTA ATG TTA ATT GCA GGA ATT GTC ATT TGT GCA	541					
Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala						
	145	150	155			
TTT TGG GTG TAC AGA CAT CAC AAG ATG GCC TAC CCT CCT GTA CTT GTT	589					
Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val						
160	165	170				
CCT ACT CAA GAC CCA GGA CCA CCC CCA CCT TCC CCA TTA CTA GGG TTG	637					
Pro Thr Gln Asp Pro Gly Pro Pro Pro Ser Pro TTA Leu Leu Gly Leu						
175	180	185				
AAG CCA TTG CAG CTG TTA GAA GTG AAA GCA AGG GGA AGA TTT GGT TGT	685					
Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys						
190	195	200	205			
GTC TGG AAA GCC CAG TTG CTC AAT GAA TAT GTG GCT GTC AAA ATA TTT	733					
Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe						
	210	215	220			

CCA Pro	ATA Ile	CAG Gln	GAC Asp 225	AAA Lys	CAG Gln	TCC Ser	TGG Trp	CAG Gln 230	AAT Asn	GAA Glu	TAT Tyr	GAA Glu	GTC Val 235	TAT Tyr	AGT Ser	781
CTA Leu	CCT Pro	GGA Gly 240	ATG Met	AAG Lys	CAT His	GAG Glu	AAC Asn 245	ATA Ile	CTA Leu	CAG Gln	TTC Phe	ATT Ile 250	GGT Gly	GCA Ala	GAG Glu	829
AAA Lys	AGA Arg 255	GGC Gly	ACC Thr	AGT Ser	GTG Val	GAT Asp 260	GTG Val	GAC Asp	CTG Leu	TGG Trp	CTA Leu 265	ATC Ile	ACA Thr	GCA Ala	TTT Phe	877
CAT His 270	GAA Glu	AAG Lys	GGC Gly	TCA Ser	CTG Leu 275	TCA Ser	GAC Asp	TTT Phe	CTT Leu	AAG Lys 280	GCT Ala	AAT Asn	GTG Val	GTC Val	TCT Ser 285	925
TGG Trp	AAT Asn	GAA Glu	CTT Leu	TGT Cys 290	CAT His	ATT Ile	GCA Ala	GAA Glu	ACC Thr 295	ATG Met	GCT Ala	AGA Arg	GGA Gly	TTG Leu 300	GCA Ala	973
TAT Tyr	TTA Leu	CAT His	GAG Glu 305	GAT Asp	ATA Ile	CCT Pro	GGC Gly	TTA Leu 310	AAA Lys	GAT Asp	GGC Gly	CAC His	AAG Lys 315	CCT Pro	GCA Ala	1021
ATC Ile	TCT Ser	CAC His 320	AGG Arg	GAC Asp	ATC Ile	AAA Lys	AGT Ser 325	AAA Lys	AAT Asn	GTG Val	CTG Leu	TTG Leu 330	AAA Lys	AAC Asn	AAT Asn	1069
CTG Leu	ACA Thr 335	GCT Ala	TGC Cys	ATT Ile	GCT Ala	GAC Asp 340	TTT Phe	GGG Gly	TTG Leu	GCC Ala	TTA Leu 345	AAG Lys	TTC Phe	GAG Glu	GCT Ala	1117
GGC Gly 350	AAG Lys	TCT Ser	GCA Ala	GGT Gly	GAC Asp 355	ACC Thr	CAT His	GGG Gly	CAG Gln	GTT Val 360	GGT Gly	ACC Thr	CGG Arg	AGG Arg	TAT Tyr 365	1165
ATG Met	GCT Ala	CCA Pro	GAG Glu	GTG Val 370	TTG Leu	GAG Glu	GGT Gly	GCT Ala	ATA Ile 375	AAC Asn	TTC Phe	CAA Gln	AGG Arg	GAC Asp 380	GCA Ala	1213
TTT Phe	CTG Leu	AGG Arg	ATA Ile 385	GAT Asp	ATG Met	TAC Tyr	GCC Ala	ATG Met 390	GGA Gly	TTA Leu	GTC Val	CTA Leu	TGG Trp 395	GAA Glu	TTG Leu	1261
GCT Ala	TCT Ser	CGT Arg 400	TGC Cys	ACT Thr	GCT Ala	GCA Ala	GAT Asp 405	GGA Gly	CCC Pro	GTA Val	GAT Asp	GAG Glu 410	TAC Tyr	ATG Met	TTA Leu	1309
CCA Pro	TTT Phe 415	GAG Glu	GAA Glu	GAA Glu	ATT Ile	GGC Gly 420	CAG Gln	CAT His	CCA Pro	TCT Ser	CTT Leu 425	GAA Glu	GAT Asp	ATG Met	CAG Gln	1357
GAA Glu 430	GTT Val	GTT Val	GTG Val	CAT His	AAA Lys 435	AAA Lys	AAG Lys	AGG Arg	CCT Pro	GTT Val 440	TTA Leu	AGA Arg	GAT Asp	TAT Tyr	TGG Trp 445	1405
CAG Gln	AAA Lys	CAT His	GCA Ala	GGA Gly 450	ATG Met	GCA Ala	ATG Met	CTC Leu	TGT Cys 455	GAA Glu	ACG Thr	ATA Ile	GAA Glu	GAA Glu 460	TGT Cys	1453
TGG Trp	GAT Asp	CAT His	GAT Asp 465	GCA Ala	GAA Glu	GCC Ala	AGG Arg	TTA Leu 470	TCA Ser	GCT Ala	GGA Gly	TGT Cys	GTA Val 475	GGT Gly	GAA Glu	1501
AGA Arg	ATT Ile	ACT Thr 480	CAG Gln	ATG Met	CAA Gln	AGA Arg	CTA Leu 485	ACA Thr	AAT Asn	ATC Ile	ATT Ile	ACT Thr 490	ACA Thr	GAG Glu	GAC Asp	1549

ATT GTA ACA GTG GTC ACA ATG GTG ACA AAT GTT GAC TTT CCT CCC AAA 1597
 Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
 495 500 505

GAA TCT AGT CTA TGATGGTGGC ACCGTCTGTA CACACTGAGG ACTGGGACTC 1649
 Glu Ser Ser Leu
 510

TGAACTGGAG CTGCTAAGCT AAGGAAAGTG CTTAGTTGAT TTTCTGTGTG AAATGAGTAG 1709
 GATGCCTCCA GGACATGTAC GCAAGCAGCC CCTTGTGGAA AGCATGGATC TGGGAGATGG 1769
 ATCTGGGAAA CTTACTGCAT CGTCTGCAGC ACAGATATGA AGAGGAGTCT AAGGGAAAAG 1829
 CTGCAAACTG TAAAGAACTT CTGAAAATGT ACTCGAAGAA TGTGGCCCTC TCCAAATCAA 1889
 GGATCTTTTG GACCTGGCTA ATCAAGTATT TGCAAACTG ACATCAGATT TCTTAATGTC 1949
 TGTCAGAAGA CACTAATTCC TTAAATGAAC TACTGCTATT TTTTAAAT GAAAACTTT 2009
 TCATTTTCAGA TTTTAAAAG GGTAACTTTT TATTGCATTT GCTGTTGTTT CTATAAATGA 2069
 CTATTGTAAT GCCAACATGA CACAGCTTGT GAATGTGTAG TGTGCTGCTG TTCTGTGTAC 2129
 ATAGTCATCA AAGTGGGGTA CAGTAAAGAG GCTTCCAAGC ATTACTTTAA CCTCCCTCAA 2189
 CAAGGTATAC CTCAGTTCCA CGGTTGTAA ATTATAAAAT TGAAAACACT AACAGAATTT 2249
 GAATAAATCA GTCCATGTTT TATAACAAGG TTAATTACAA ATTCAGTGTG TTATTTAAGA 2309
 AAAAAATGGTA AGCTATGCTT AGTGCCAATA GTAAGTGGCT ATTTGTAAAG CAGTGTTTTA 2369
 GCTTTTCTTC TACTGGCTTG TAATTTAGGG AAAACAAGTG CTGTCTTTGA AATGGAAAAG 2429
 AATATGGTGT CACCCTACCC CCCATACTTA TATCAAGGTC CCAAAATATT CTTTTCATT 2489
 TCAAAGACAG CACTTTGAAA ACCCTAAATT ACAAGCCAGT AGAAGAAAAG CTAAAACACG 2549
 CTTTACAAAT AGCC 2563

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
 1 5 10 15

Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
 20 25 30

Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu
 35 40 45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
 50 55 60

Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
 65 70 75 80

Asp	Asp	Ile	Asn	Cys 85	Tyr	Asp	Arg	Thr	Asp 90	Cys	Ile	Glu	Lys	Lys 95	Asp
Ser	Pro	Glu	Val 100	Tyr	Phe	Cys	Cys	Cys 105	Glu	Gly	Asn	Met	Cys 110	Asn	Glu
Lys	Phe	Ser 115	Tyr	Phe	Pro	Glu	Met 120	Glu	Val	Thr	Gln	Pro 125	Thr	Ser	Asn
Pro	Val 130	Thr	Pro	Lys	Pro	Pro 135	Tyr	Tyr	Asn	Ile	Leu 140	Leu	Tyr	Ser	Leu
Val 145	Pro	Leu	Met	Leu	Ile 150	Ala	Gly	Ile	Val	Ile 155	Cys	Ala	Phe	Trp	Val 160
Tyr	Arg	His	His	Lys 165	Met	Ala	Tyr	Pro	Pro 170	Val	Leu	Val	Pro	Thr 175	Gln
Asp	Pro	Gly	Pro 180	Pro	Pro	Pro	Ser	Pro 185	Leu	Leu	Gly	Leu	Lys 190	Pro	Leu
Gln	Leu	Leu 195	Glu	Val	Lys	Ala	Arg 200	Gly	Arg	Phe	Gly	Cys 205	Val	Trp	Lys
Ala	Gln 210	Leu	Leu	Asn	Glu	Tyr 215	Val	Ala	Val	Lys	Ile 220	Phe	Pro	Ile	Gln
Asp 225	Lys	Gln	Ser	Trp	Gln 230	Asn	Glu	Tyr	Glu	Val 235	Tyr	Ser	Leu	Pro	Gly 240
Met	Lys	His	Glu	Asn 245	Ile	Leu	Gln	Phe	Ile 250	Gly	Ala	Glu	Lys	Arg 255	Gly
Thr	Ser	Val	Asp 260	Val	Asp	Leu	Trp	Leu 265	Ile	Thr	Ala	Phe	His 270	Glu	Lys
Gly	Ser 275	Leu	Ser	Asp	Phe	Leu	Lys 280	Ala	Asn	Val	Val	Ser 285	Trp	Asn	Glu
Leu	Cys 290	His	Ile	Ala	Glu	Thr 295	Met	Ala	Arg	Gly	Leu 300	Ala	Tyr	Leu	His
Glu 305	Asp	Ile	Pro	Gly	Leu 310	Lys	Asp	Gly	His	Lys 315	Pro	Ala	Ile	Ser	His 320
Arg	Asp	Ile	Lys	Ser 325	Lys	Asn	Val	Leu	Leu 330	Lys	Asn	Asn	Leu	Thr 335	Ala
Cys	Ile	Ala	Asp 340	Phe	Gly	Leu	Ala	Leu 345	Lys	Phe	Glu	Ala	Gly 350	Lys	Ser
Ala	Gly	Asp 355	Thr	His	Gly	Gln	Val 360	Gly	Thr	Arg	Arg	Tyr 365	Met	Ala	Pro
Glu 370	Val	Leu	Glu	Gly	Ala	Ile 375	Asn	Phe	Gln	Arg	Asp 380	Ala	Phe	Leu	Arg
Ile 385	Asp	Met	Tyr	Ala	Met 390	Gly	Leu	Val	Leu	Trp 395	Glu	Leu	Ala	Ser	Arg 400
Cys	Thr	Ala	Ala	Asp 405	Gly	Pro	Val	Asp	Glu 410	Tyr	Met	Leu	Pro	Phe 415	Glu
Glu	Glu	Ile	Gly 420	Gln	His	Pro	Ser	Leu 425	Glu	Asp	Met	Gln	Glu 430	Val	Val

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: XACTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCCCCACAC	AGTGCACTGA	ATAATAGCCG	GTGCGGCCCC	TCCCCTCTTT	CCCTGGCAGT	60
TGTGTATCTG	TCACATTGAA	GTTTGGGCTC	CTGTGAGTCT	GAGCCTCCCC	CTGTGTCTCA	120
TGTGAAGCTG	CTGCTGCAGA	AGGTGGAGTC	GTTGCATGAG	GGTGGGGGGA	GTCTGCTGCTG	180
TTTGATCTGC	CTCTGCTCCC	CATTCACT	CTCATTTCAT	TCCCACGGAT	CCACATTACA	240
ACTCGCCTTT	AACCCCTTCC	CTGGCGGAGC	CCACGCGTCT	TTCATCCCTC	CTGCCGCGGC	300
CGCTGAGCGA	CCAGAGCGCG	ACATTGTTGC	GGCGGGGGAT	TGGGCGACAT	TGTTGCGAAT	360
AATCGGAGCT	GCTGGGGGGG	AACTGATACA	ACGTTGCGAC	TGTAAAGGAA	TTAACTCGGC	420
CGAATGGGAT	TTTATCTGTG	TCGGTGAGAG	AAGCGGATCC	CAGGAGC	ATG GGG GCG Met Gly Ala 1	476
TCT GTA GCG CTG ACT TTT CTA CTT CTT CTT GCA ACT TTC CGC GCA GGC						524
Ser Val Ala Leu Thr Phe Leu Leu Leu Leu Ala Thr Phe Arg Ala Gly						
5	10	15				
TCA GGA CAC GAT GAA GTG GAG ACA AGA GAG TGC ATC TAT TAC AAT GCC						572
Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr Tyr Asn Ala						
20	25	30	35			

AAC TGG GAA CTG GAG AAG ACC AAC CAA AGT GGG GTG GAA AGC TGC GAA Asn Trp Glu Leu Glu Lys Thr Asn Gln Ser Gly Val Glu Ser Cys Glu 40 45 50	620
GGG GAA AAG GAC AAG CGA CTC CAC TGT TAC GCG TCT TGG AGG AAC AAT Gly Glu Lys Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg Asn Asn 55 60 65	668
TCG GGC TTC ATA GAG CTG GTG AAA AAA GGA TGC TGG CTG GAT GAC TTC Ser Gly Phe Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp Asp Phe 70 75 80	716
AAC TGT TAT GAC AGA CAG GAA TGT ATT GCC AAG GAA GAA AAC CCC CAA Asn Cys Tyr Asp Arg Gln Glu Cys Ile Ala Lys Glu Glu Asn Pro Gln 85 90 95	764
GTC TTT TTC TGC TGC TGC GAG GGA AAC TAC TGC AAC AAG AAA TTT ACT Val Phe Phe Cys Cys Cys Glu Gly Asn Tyr Cys Asn Lys Lys Phe Thr 100 105 110 115	812
CAT TTG CCT GAA GTC GAA ACA TTT GAT CCG AAG CCC CAG CCG TCA GCC His Leu Pro Glu Val Glu Thr Phe Asp Pro Lys Pro Gln Pro Ser Ala 120 125 130	860
TCC GTA CTG AAC ATT CTG ATC TAT TCC CTG CTT CCA ATT GTT GGT CTT Ser Val Leu Asn Ile Leu Ile Tyr Ser Leu Leu Pro Ile Val Gly Leu 135 140 145	908
TCC ATG GCA ATT CTC CTG GCG TTC TGG ATG TAC CGT CAT CGA AAG CCT Ser Met Ala Ile Leu Leu Ala Phe Trp Met Tyr Arg His Arg Lys Pro 150 155 160	956
CCC TAC GGG CAT GTA GAG ATC AAT GAG GAC CCC GGT CTG CCC CCT CCA Pro Tyr Gly His Val Glu Ile Asn Glu Asp Pro Gly Leu Pro Pro Pro 165 170 175	1004
TCT CCT CTG GTC GGG CTG AAG CCG CTG CAG TTG CTG GAG ATA AAG GCG Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala 180 185 190 195	1052
CGA GGC CGT TTC GGT TGC GTC TGG AAA GCT CGT CTG CTG AAT GAA TAT Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Arg Leu Leu Asn Glu Tyr 200 205 210	1100
GTC GCA GTG AAA ATC TTC CCC GTG CAG GAT AAG CAG TCG TGG CAG TGT Val Ala Val Lys Ile Phe Pro Val Gln Asp Lys Gln Ser Trp Gln Cys 215 220 225	1148
GAG AAA GAG ATC TTC ACC ACG CCG GGC ATG AAA CAT GAA AAC CTA TTG Glu Lys Glu Ile Phe Thr Thr Pro Gly Met Lys His Glu Asn Leu Leu 230 235 240	1196
GAG TTC ATT GCC GCT GAG AAG AGG GGA AGC AAC CTG GAG ATG GAG CTG Glu Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Met Glu Leu 245 250 255	1244
TGG CTC ATC ACT GCA TTT CAT GAT AAG GGT TCT CTG ACG GAC TAC CTG Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu 260 265 270 275	1292
AAA GGG AAC TTG GTG AGC TGG AAT GAA CTG TGT CAC ATA ACA GAA ACA Lys Gly Asn Leu Val Ser Trp Asn Glu Leu Cys His Ile Thr Glu Thr 280 285 290	1340
ATG GCT CGT GGG CTG GCC TAC TTA CAT GAA GAT GTG CCC CGC TGT AAA Met Ala Arg Gly Leu Ala Tyr Leu His Glu Asp Val Pro Arg Cys Lys 295 300 305	1388

0042584-12100

GGT Gly	GAA Glu	GGG Gly	CAC His	AAA Lys	CCT Pro	GCA Ala	ATC Ile	GCT Ala	CAC His	AGA Arg	GAT Asp	TTT Phe	AAA Lys	AGT Ser	AAG Lys	1436	
310 315 320																	
AAT Asn	GTA Val	TTG Leu	CTA Leu	AGA Arg	AAC Asn	GAC Asp	CTG Leu	ACT Thr	GCG Ala	ATA Ile	TTA Leu	GCA Ala	GAC Asp	TTC Phe	GGG Gly	1484	
325 330 335																	
CTG Leu	GCC Ala	GTA Val	CGA Arg	TTT Phe	GAG Glu	CCT Pro	GGA Gly	AAA Lys	CCT Pro	CCG Pro	GGA Gly	GAT Asp	ACA Thr	CAC His	GGG Gly	1532	
340 345 350 355																	
CAG Gln	GTT Val	GGC Gly	ACC Thr	AGG Arg	AGG Arg	TAT Tyr	ATG Met	GCT Ala	CCT Pro	GAG Glu	GTT Val	CTA Leu	GAG Glu	GGG Gly	GCA Ala	1580	
360 365 370																	
ATT Ile	AAC Asn	TTT Phe	CAG Gln	CGA Arg	GAT Asp	TCC Ser	TTT Phe	CTC Leu	AGG Arg	ATA Ile	GAT Asp	ATG Met	TAT Tyr	GCC Ala	ATG Met	1628	
375 380 385																	
GGA Gly	CTG Leu	GTA Val	CTC Leu	TGG Trp	GAA Glu	ATA Ile	GTA Val	TCC Ser	CGA Arg	TGT Cys	ACA Thr	GCA Ala	GCA Ala	GAT Asp	GGG Gly	1676	
390 395 400																	
CCA Pro	GTA Val	GAT Asp	GAG Glu	TAT Tyr	CTG Leu	CTC Leu	CCA Pro	TTC Phe	GAA Glu	GAA Glu	GAG Glu	ATT Ile	GGG Gly	CAA Gln	CAT His	1724	
405 410 415																	
CCT Pro	TCC Ser	CTA Leu	GAG Glu	GAT Asp	CTG Leu	CAA Gln	GAA Glu	GTT Val	GTC Val	GTT Val	CAC His	AAG Lys	AAG Lys	ATA Ile	CGC Arg	1772	
420 425 430 435																	
CCT Pro	GTA Val	TTC Phe	AAA Lys	GAC Asp	CAC His	TGG Trp	CTG Leu	AAA Lys	CAC His	CCT Pro	GGT Gly	CTG Leu	GCC Ala	CAA Gln	CTG Leu	1820	
440 445 450																	
TGC Cys	GTC Val	ACC Thr	ATT Ile	GAA Glu	GAA Glu	TGC Cys	TGG Trp	GAC Asp	CAT His	GAT Asp	GCG Ala	GAA Glu	GCA Ala	CGG Arg	CTT Leu	1868	
455 460 465																	
TCG Ser	GCA Ala	GGC Gly	TGC Cys	GTA Val	GAG Glu	GAG Glu	CGT Arg	ATT Ile	TCC Ser	CAA Gln	ATC Ile	CGT Arg	AAA Lys	TCA Ser	GTG Val	1916	
470 475 480																	
AAC Asn	GGC Gly	ACT Thr	ACC Thr	TCG Ser	GAC Asp	TGC Cys	CTT Leu	GTA Val	TCC Ser	ATT Ile	GTT Val	ACA Thr	TCT Ser	GTC Val	ACC Thr	1964	
485 490 495																	
AAT Asn	GTG Val	GAC Asp	TTG Leu	CCG Pro	CCC Pro	AAA Lys	GAG Glu	TCC Ser	AGT Ser	ATC Ile	TGAGGTTTCT				TTGGTCTTTCT		2017
500 505 510																	
CAGACTCAGT GACTTTTAAA AAAAAAACTC ACGAATGCAG CTGCTATTTT ATCTTGACTT 2077																	
TTTAAATATTT TTTTCTTGG ATTTTACTTG GATCGGATCA ATTTACCAGC ACGTCATTCTG 2137																	
AAAGTATTAA AAAAAAAAAA CAAAACAAAA AAGCAAAAAC AGACATCTCA GCAAGCATTC 2197																	
AGGTGCCGAC TTATGAATGC CAATAGGTGC AGGAACTTCA GAACCTCAAC AAACCTCATTT 2257																	
CTAGAGAATG TTCTCCTGGT TTCCTTTATC TCAGAAGAGG ACCCATAGGA AAACACCTAA 2317																	
GTCAAGCAAA TGCTGCAG 2335																	

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 510 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1	Gly	Ala	Ser	Val 5	Ala	Leu	Thr	Phe	Leu 10	Leu	Leu	Leu	Ala	Thr 15	Phe
Arg	Ala	Gly	Ser 20	Gly	His	Asp	Glu	Val 25	Glu	Thr	Arg	Glu	Cys 30	Ile	Tyr
Tyr	Asn	Ala 35	Asn	Trp	Glu	Leu	Glu 40	Lys	Thr	Asn	Gln	Ser 45	Gly	Val	Glu
Ser	Cys 50	Glu	Gly	Glu	Lys	Asp 55	Lys	Arg	Leu	His	Cys 60	Tyr	Ala	Ser	Trp
Arg 65	Asn	Asn	Ser	Gly	Phe 70	Ile	Glu	Leu	Val	Lys 75	Lys	Gly	Cys	Trp	Leu 80
Asp	Asp	Phe	Asn	Cys 85	Tyr	Asp	Arg	Gln	Glu 90	Cys	Ile	Ala	Lys	Glu 95	Glu
Asn	Pro	Gln	Val 100	Phe	Phe	Cys	Cys	Cys 105	Glu	Gly	Asn	Tyr	Cys 110	Asn	Lys
Lys	Phe	Thr 115	His	Leu	Pro	Glu	Val 120	Glu	Thr	Phe	Asp	Pro 125	Lys	Pro	Gln
Pro	Ser 130	Ala	Ser	Val	Leu	Asn 135	Ile	Leu	Ile	Tyr	Ser 140	Leu	Leu	Pro	Ile
Val 145	Gly	Leu	Ser	Met	Ala 150	Ile	Leu	Leu	Ala	Phe 155	Trp	Met	Tyr	Arg	His 160
Arg	Lys	Pro	Pro	Tyr 165	Gly	His	Val	Glu	Ile 170	Asn	Glu	Asp	Pro	Gly 175	Leu
Pro	Pro	Pro	Ser 180	Pro	Leu	Val	Gly	Leu 185	Lys	Pro	Leu	Gln	Leu 190	Leu	Glu
Ile	Lys	Ala 195	Arg	Gly	Arg	Phe	Gly 200	Cys	Val	Trp	Lys	Ala 205	Arg	Leu	Leu
Asn	Glu 210	Tyr	Val	Ala	Val	Lys 215	Ile	Phe	Pro	Val	Gln 220	Asp	Lys	Gln	Ser
Trp 225	Gln	Cys	Glu	Lys	Glu 230	Ile	Phe	Thr	Thr	Pro 235	Gly	Met	Lys	His	Glu 240
Asn	Leu	Leu	Glu	Phe 245	Ile	Ala	Ala	Glu	Lys 250	Arg	Gly	Ser	Asn	Leu 255	Glu
Met	Glu	Leu	Trp 260	Leu	Ile	Thr	Ala	Phe 265	His	Asp	Lys	Gly	Ser 270	Leu	Thr
Asp	Tyr	Leu 275	Lys	Gly	Asn	Leu	Val 280	Ser	Trp	Asn	Glu	Leu 285	Cys	His	Ile
Thr	Glu 290	Thr	Met	Ala	Arg	Gly 295	Leu	Ala	Tyr	Leu	His 300	Glu	Asp	Val	Pro

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
Asp Leu Lys Pro Glu Asn
1 5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "Xaa at position 2 is either
"Thr" or "Ser"."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "Xaa a position 5 is either
"Tyr" or "Phe"."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Ile Lys Ser Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Thr Arg Arg Tyr Met
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Leu Ala Ala Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is either
"Ile" or "Val"."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is either
"Lys" or "Arg"."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is either
"Thr" or "Met"."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Pro Xaa Xaa Trp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 72..1553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCCGGAAC TTCAAAGCGC GCTGCGGCGG CGCTCTGGA CCCCAGGCC TTGCACCGCC

60

GCGGGGTGGC C ATG ACC CCA GCG CGC CGC TCC GCA CTG AGC CTG GCC CTC
Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu

110

1

5

10

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1. 姓名: 张三
 2. 性别: 男
 3. 年龄: 25
 4. 职业: 教师
 5. 籍贯: 湖南
 6. 民族: 汉族
 7. 婚姻状况: 已婚
 8. 子女情况: 一子一女
 9. 健康状况: 良好
 10. 兴趣爱好: 读书、运动
 11. 教育程度: 本科
 12. 工作单位: 某某中学
 13. 联系电话: 13800138000
 14. 电子邮箱: zhangsan@example.com
 15. 身份证号: 430101199801010001

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ATA GTG ACC GTG GCT GGA ATG GTC AAG TTG GCG CTT TCA ATA GCG AGT Ile Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser	974
290 295 300	
GGT CTG GCT CAC CTA CAC ATG GAG ATC GTG GGC ACT CAA GGT AAG CCT Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro	1022
305 310 315	
GCT ATT GCT CAC CGA GAT ATA AAG TCA AAG AAT ATC TTA GTC AAA AAG Ala Ile Ala His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys	1070
320 325 330	
TGT GAC ACT TGT GCC ATA GCT GAC TTA GGG CTG GCT GTG AAA CAT GAT Cys Asp Thr Cys Ala Ile Ala Asp Leu Gly Leu Val Lys His Asp	1118
335 340 345	
TCT ATC ATG AAC ACT ATA GAT ATA CCC CAG AAT CCT AAA GTG GGA ACC Ser Ile Met Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr	1166
350 355 360 365	
AAG AGG TAT ATG GCT CCC GAA ATG CTT GAT GAT ACA ATG AAC GTC AAC Lys Arg Tyr Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn	1214
370 375 380	
ATC TTT GAG TCC TTC AAG CGA GCT GAC ATC TAT TCG GTG GGG CTG GTT Ile Phe Glu Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val	1262
385 390 395	
TAC TGG GAA ATA GCT CGA AGG TGT TCA GTT GGA GGA CTT GTT GAA GAG Tyr Trp Glu Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu	1310
400 405 410	
TAC CAG TTG CCT TAT TAT GAC ATG GTG CCT TCA GAT CCT TCC ATA GAG Tyr Gln Leu Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu	1358
415 420 425	
GAA ATG AGG AAG GTC GTT TGT GAT CAG AAA CTG CGA CCA AAT CTC CCA Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro	1406
430 435 440 445	
AAC CAG TGG CAA AGC TGT GAG GCG CTC CGG GTC ATG GGA AGA ATA ATG Asn Gln Trp Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met	1454
450 455 460	
CGT GAG TGC TGG TAT GCC AAC GGG GCA GCT CGC CTG ACC GCC CTG CGC Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg	1502
465 470 475	
GTG AAG AAG ACC ATT TCT CAG CTG TGT GTC AAG GAA GAC TGT AAG GCC Val Lys Lys Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala	1550
480 485 490	
TAAGGATACA GGCGACGGGA AAGCCCTCAC CACTCTCTTT CATGTCTCCT GC	1602

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:12:

Met	Thr	Pro	Ala	Arg	Arg	Ser	Ala	Leu	Ser	Leu	Ala	Leu	Leu	Leu	Val
1				5					10						15
Ala	Leu	Ala	Ser	Asp	Leu	Ala	Ala	Gly	Leu	Lys	Cys	Val	Cys	Leu	Leu
			20					25					30		
Cys	Asp	Ser	Ser	Asn	Phe	Thr	Cys	Gln	Thr	Glu	Gly	Ala	Cys	Trp	Ala
		35					40					45			
Ser	Val	Met	Leu	Thr	Asn	Gly	Lys	Glu	Gln	Val	Ser	Lys	Ser	Cys	Val
	50					55					60				
Ser	Leu	Pro	Glu	Leu	Asn	Ala	Gln	Val	Phe	Cys	His	Ser	Ser	Asn	Asn
	65				70					75					80
Val	Thr	Lys	Thr	Glu	Cys	Cys	Phe	Thr	Asp	Phe	Cys	Asn	Asn	Ile	Thr
				85					90					95	
Gln	His	Leu	Pro	Thr	Ala	Ser	Pro	Asp	Ala	Pro	Arg	Leu	Gly	Pro	Thr
			100					105					110		
Glu	Leu	Thr	Val	Val	Ile	Thr	Val	Pro	Val	Cys	Leu	Leu	Ser	Ile	Ala
	115						120					125			
Ala	Met	Leu	Thr	Ile	Trp	Ala	Cys	Gln	Asp	Arg	Gln	Cys	Thr	Tyr	Arg
	130					135					140				
Lys	Thr	Lys	Arg	His	Asn	Val	Glu	Glu	Pro	Leu	Ala	Glu	Tyr	Ser	Leu
	145				150					155					160
Val	Asn	Ala	Gly	Lys	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Ala	Thr	Ala
				165					170					175	
Ser	Gly	Ser	Gly	Ser	Gly	Pro	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala
			180					185					190		
Arg	Thr	Ile	Val	Leu	Gln	Glu	Ile	Val	Gly	Lys	Gly	Arg	Phe	Gly	Glu
		195				200						205			
Val	Trp	His	Gly	Arg	Trp	Cys	Gly	Glu	Asp	Val	Ala	Val	Lys	Ile	Phe
	210					215					220				
Ser	Ser	Arg	Asp	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln
				225	230					235					240
Thr	Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp
				245					250					255	
Asn	Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Glu	Tyr
			260					265					270		
His	Glu	Gln	Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Asn	Arg	Asn	Ile	Val	Thr
		275					280					285			
Val	Ala	Gly	Met	Val	Lys	Leu	Ala	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala
	290					295					300				

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
305 310 315 320
His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Asp Thr
325 330 335
Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Met
340 345 350
Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
355 360 365
Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
370 375 380
Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
385 390 395 400
Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu Tyr Gln Leu
405 410 415
Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
420 425 430
Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro Asn Gln Trp
435 440 445
Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
450 455 460
Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Val Lys Lys
465 470 475 480
Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
485 490

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGGATCCGT NGCNGTNAAR ATHTTYCC

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGGATCCYT CNGGNGCCAT RTANCKYCTN GTNCC

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